



Figure S5. Correlation of RNA-Seq and ChIP-Seq data for the subsets of genes related to cell cycle (**A**) and myogenic factors (**B**), and differentially expressed genes within the cardiac muscle contraction KEGG pathway (dre04260)(**C**) and lysosome KEGG pathway (dre04142)(**D**). Gene expression is plotted using the log₁₀ of Fragments Per Kilobase of transcript per Million mapped reads (FPKM) and this is plotted against the average peak value for each histone mark at each time point. Statistical significance is reported using Pearson's *r* value of correlation for data sets which also have a $P < 0.05$.